

09988745-112001

10 30 50
CTAGAGCTAGCAGGAGTAACTCTCATGGAACCTTGGAACCATTTCTTCAATTGAATTTCA
70 90 110
GGGCACATTTGAATCAGTACCCAGGGGCACTGTACTATGCTCCCAGCTGGACCTTAGTTT
130 150 170
CCTCCTCCTCGTTTCACCTGTGAGTAATTAACAGACAAAATTTTTTTTTTTTTTTTTT
190 210 230
TTTTTTTTTTTTTTTGGCCCTCCAGTGGAGAAGGTGGCCAGTTCTCAGACAGAGGAAGAGT
250 270 290
AGAAATCATAAATGAGAGCTGTCTTCATCCAAGGTGCTGAAGAGCACCTGCGGCATTCT
M R A V F I Q G A E E H P A A F C 17
310 330 350
GCTACCAGGTGAATGGGTCTTGCCCCAGGACAGTACATACTCTGGGCATCCAGTTGGTCA
Y Q V N G S C P R T V H T L S I Q L V I
370 390 410
TCTACCTGACCTGTGCAGCAGGCATGCTGATTATCGTGCTAGGGAATGTATTTGTGGCAT
Y L T C A A G M L I I V L G N V F V A F
430 450 470
TTGCTGTGTCTTACTTCAAAGCGCTTCACACGCCCACCAACTTCCTGCTGCTCTCCCTGG
A V S Y F K A L H T P T N F L L L S L A
490 510 530
CCCTGGCTGACATGTTTCTGGGTCTGCTGGTGTGCCCCCTCAGCACCATTCGCTCAGTGG
L A D M F L G L L V L P L S T I R S V E
550 570 590
AGAGCTGCTGGTTCTTCGGGGACTTCCTCTGCCGCTGCACACCTACCTGGACACCCTCT
S C W F F G D F L C R L H T Y L D T L F
610 630 650
TCTGCCTCACCTCCATCTTCCATCTCTGTTTCATTTCCATTGACCGCCACTGTGCCATCT
C L T S I F H L C F I S I D R H C A I C
670 690 710
GTGACCCCTGCTCTATCCCTCCAAGTTCACAGTGAGGGTGGCTCTCAGGTACATCCTGG
D P L L Y P S K F T V R V A L R Y I L A
730 750 770
CAGGATGGGGGTGCCCCGAGCATACTTCGTTATTCTCTACACAGATGTGGTAGAGA
G W G V P A A Y T S L F L Y T D V V E T
790 810 830
CAAGGCTCAGCCAGTGGCTGGAAGAGATGCCTTGTGTGGGCAGTTGCCAGCTGCTGCTCA
R L S Q W L E E M P C V G S C Q L L L N
850 870 890
ATAAATTTTGGGGCTGGTTAAACTTCCCTTTGTTCTTTGTCCCCTGCCTCATTATGATCA
K F W G W L N F P L F F V P C L I M I S
910 930 950
GCTTGTATGTGAAGATCTTTGTGGTTGCTACCAGACAGGCTCAGCAGATTACCACATTGA
L Y V K I F V V A T R Q A Q Q I T T L S
970 990 1010
GCAAAAGCCTGGCTGGGGCTGCCAAGCATGAGAGAAAAGCTGCCAAGACCCTGGGCATTG
K S L A G A A K H E R K A A K T L G I V
1030 1050 1070
TTGTGGGCATATACCTCTTGTGCTGGCTGCCCTTCACCATAGACACGATGGTCGACAGCC
V G I Y L L C W L P F T I D T M V D S L
1090 1110 1130
TCCTTCACTTTATCACACCCCCACTGGTCTTTGACATCTTTATCTGGTTTGCTTACTTCA
L H F I T P P L V F D I F I W F A Y F N
1150 1170 1190
ACTCAGCCTGCAACCCCATCATCTATGTCTTTTCTTACCAGTGGTTTCGGAAGGCACTGA
S A C N P I I Y V F S Y Q W F R K A L K
1210 1230 1250
AACTCACACTGAGCCAGAAGGTCTTCTACCGCAGACACGCACTGTTGATTTGTACCAAG
L T L S Q K V F S P Q T R T V D L Y Q E
1270 1290 1310
AATGATTCCTTCTACTAAATGCAGGCAAGGAGTAGGACCTCACAGGAAAGATAAGTGGA
*
1330 1350 1370
CTGTGACCGCGGGCTGTGTGGTGTGAGTTTGTGGGCATGCTTCCAGGACAGCATGGGT

325800-451

FIGURE

1 1/1

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Homology Comparison **HDGRC02 X Mu.β-1 Adrenoreceptor**

Percent Similarity: 55.864 Percent Identity: 32.099

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3  AVFIQGAEEHPAAFCYQVNGSCPRTVH.TLGIQLVIYLTCAAGMLIIVLG 51
| :: |...: . . :||. | . : | |::|:: |. :|::|::|
30  ARLLVLASPPASLLPPASEGSAPLSQQWTAGMGLLVALI....VLLIVVG 75

52  NVFVAFVSYFKALHTPTNELLSSALADMFLGLLVLPLSTIRSVESCWF 101
||:| .|:: . |:: ||:::|||| |:::|||||:|::: . | : |
76  NVLVIVAIKTPRLQTLTNLFIMSLASADLVMGLLVVFPGATIVVWGRWE 125

102 FGDFLCRLHTYLDTLFCLTSIFHLCFISIDRHCAICDPLLYPSKFTVRVA 151
:|.::| | | :|. | . .|| | |.::| |. | |.::| |. | :|
126 YGSFFCELWTSVDVLCVTASIELTLCVIALDRYLAITSPFRYQSLLTRARA 175

152 LRYILAGWGVPAAYTSLFLYTDVVETRLSQWLEEMPCVG...SCQLLLNK 198
. : .|.::| : : : : : : : .|. | . :|::| :
176 RALVCTVWAISAL...VSFLPILMHWWRAESDEARRCYNDPKCCDFVTNR 222

199 FWGWLNFPL.FFVPCLIMISLYVKIFVVATRQAQQITLSKSLAGA.... 243
:: . : :|::| || :|:::| | :|...|.. :::| :
223 AYAIASSVVSFYVPLCIMAFAVYLRVFREAQKQVKKIDSCERRFLGGPARP 272

244 .....AKHERKAAKTLGIVVGIY 261
| :|.|| |||||:|::
273 PSPEPSPSPGPPRPADSLANGRSSKRRPSRLVALREQKALKTLGIIMGVF 322

262 LLCWLPFTIDTMVDSLHFITPPLVFDIFIWFAYFNSACNPIIYVFSYQW 311
||||| :::|...: : .|. :| :| |::| ||| |||||. | :
323 TLCWLPFFLANVVKAHFDLVPDRLVFFFNWLGYSANSAFNPIIYCRSPDF 372

312 FRKALKLTLSQKVFSPTQTRTVD 333
: :| ::: . . |...
373 RKAQRLCCARRAACRRRAAH 394

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0988745-1001

FIGURE 2 1/1
325800-451

2 of 3

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8  GAEHPAAFCYQVNGSCPRTVHTLGIQLVILYLTCAAGMLIIVLGNVFAF 57
   : : : . . . . . : . | | . . . . . : . . . . . : : : | | : : :
10 DDDLERQNWSPFNGSDGKADRPYNYATLLT..LLIAVIVFGNVLVCM 57

58 AVSYFKAIHTPTNFLLLSLALADMFLGLLVLPLSTIRSVESCWFFGDFLC 107
   | | | | | : | : | : | : | : | : | : | : | : | : | : | : |
58 AVSREKALQTTTNYLIVSLAVADLLVATLVMPWVYVLEVVGWKFSSRIHC 107

108 RLHTYLDTLFCLTSIFHLCFISIDRHCAICDPLLYPSKFTVRVALRYILA 157
   : . | | : : | . | | : : | | | | | . : . | : | . : : : :
108 DIFVTLDVMMCTASIILNLCAISIDRYTAVAMPMLYNTRYSSKRRVTVMIS 157

158 .GWGVPAAYTSLFLYTDTVETRLSQWLEEMPCVGCQLLLNKFWGWLNFP 206
   . | : . . . : : | : . | . : : . . . . . : : : : :
158 IVWVLSFTISCPLLFG.....LNNADQNECIIANPAFVV.....YSSIV 196

207 LFFVPCCLIMISLYVKIFVVATRQAQQITT.....LSKSLAGAAKH 246
   | : | | : : : : | : | : | | . . . . | . . | : | : :
197 SFYVPFIVTLLVYIKIYIVLRRRRKRVTNKRSSRAFRAHLRAPLKEAARR 246

247 .....ERKAAKTL 254
   | : | | . . |
297 EKNGHAKDHPKIAKIFEIQTMPNGKTRTSLKTMSRRKLSQQKEKKATQML 346

255 GIVVGIYLLCWL PFTIDTMVDSL LHFITPPLVFDIFIWFAYFNSACNP II 304
   : | | : : : : | | | | | . : : . . | | : : . | : : | | | |
347 AIVLGVFIICWLPFFITHILNIHCD CNIPPVLYSAFTWLG VNSAVNP II 396

305 YVFSYQWFRKALKLTL 320
   | . . . | | | : . |
397 YTTFNIEFRKAFLKIL 412

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FIGURE 3
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3, 1, 3